

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/602,043  
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## RAW SEQUENCE LISTING

DATE: 07/05/2006

PATENT APPLICATION: US/10/602,043

TIME: 12:52:36

Input Set : N:\Crf3\RULE60\10602043.RAW.txt

Output Set: N:\CRF4\07052006\J602043.raw

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1 <110> APPLICANT: Wei et al.
2 <120> TITLE OF INVENTION: Human DNA Topoisomerase 1 Alpha
3 <130> FILE REFERENCE: PF118D3
4 <140> CURRENT APPLICATION NUMBER: US/10/602,043
5 <141> CURRENT FILING DATE: 2003-06-24
6 <150> PRIOR APPLICATION NUMBER: US/09/871,615
7 <151> PRIOR FILING DATE: 2001-06-04
8 <150> PRIOR APPLICATION NUMBER: 09/325,430
9 <151> PRIOR FILING DATE: 1999-06-04
10 <150> PRIOR APPLICATION NUMBER: 09/033,153
11 <151> PRIOR FILING DATE: 1998-03-02
12 <150> PRIOR APPLICATION NUMBER: 08/458,477
13 <151> PRIOR FILING DATE: 1995-06-02
14 <150> PRIOR APPLICATION NUMBER: PCT/US94/05701
15 <151> PRIOR FILING DATE: 1994-05-18
16 <160> NUMBER OF SEQ ID NOS: 5
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1917
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
24      gcagatgctg  gtggtgcggc  tgctgcggct  ccgggcggct  ctgacgctgc  tcggggaggt  60
25      cccccgcgc  ccggcctccc  ggggtgtccc  gggctcgcgc  aggacgcaga  agggcagtgg  120
26      agccaggtgg  gagaaggaga  agcacgaaga  cggggtgaag  tggagacagc  tggagcacia  180
27      gggcccgta  ttcgcacccc  catacgagcc  ccttcccgac  ggagtgcgtt  tcttctatga  240
28      aggaaggcct  gtgagattga  gcgtgccagc  ggaggaggtc  cccacttttt  atgggaggat  300
29      gttagatcat  gaatacacia  caaaggaggt  tttccggaag  aacttcttca  atgactggcg  360
30      aaaggaaatg  gcggtggaag  agagggaagt  catcaagagc  ctggacaagt  gtgacttcac  420
31      ggagatccac  agatactttg  tggacaaggc  cgcagcccgc  aaagtcctga  gcagggagga  480
32      gaagcagaag  ctaaaagaag  aggcagaaaa  acttcagcaa  gagttcggct  actgtatttt  540
33      agatggtcac  caagaaaaaa  taggcaactt  caagattgag  ccgcctggct  tggtccgtgg  600
34      ccgtggcgac  catcccaaga  tggggatgct  gaagagaagg  atcacgccag  aggatgtggt  660
35      tatcaactgc  agcagggaat  cgaagatccc  cgagccgccc  gcggggcacc  agtggaaagg  720
36      ggtgcgctcc  gataacaccg  tcacgtggct  ggcagcttgg  accgagagcg  ttcagaactc  780
37      catcaagtac  atcatgctga  acccttgctc  gaagctgaag  ggggagacag  cttggcagaa  840
38      gtttgaaaca  gctcgacgcc  tgcggggatt  tgtggacgag  atccgctccc  agtaccgggc  900
39      tgactggaag  tctcgggaaa  tgaagacgag  acagcgggcg  gtggccctgt  atttcacga  960
40      taagtggca  ctgagagcag  gaaatgagaa  ggaggacggg  gaggcggccg  acaccgtggg  1020
41      ctgctgttcc  ctccgcgtgg  agcagctcca  gctgcacccc  gaggcgatg  gttgccaaca  1080
42      cgtggtggaa  tttgacttcc  tggggaagga  ctgcattccg  tactacaaca  gaggcccggt  1140
43      ggagaagccg  gtgtacaaga  acttacagct  ctttatggag  aacaaggacc  cccgggacga  1200
44      cctcttcgac  aggctgacca  cgaccagcct  gaacaagcac  ctccaggagc  tgatggacgg  1260

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45      gctgacggcc aaggtgttcc ggacctacaa cgcctccatc actctgcagg agcagctgcg 1320
46      ggccctgacg cgcgccgagg acagcatagc agctaagatc ttatcctaca accgagccaa 1380
47      ccgagtcgtg gccattctct gcaaccatca gcgagcaacc cccagtacgt tcgagaagtc 1440
48      gatgcagaat ctccagacga agatccaggc aaagaaggag caggtggctg agggccagggc 1500
49      agagctgagg agggcgaggg ctgagcacia agcccaaggg gatggcaagt ccaggagtgt 1560
50      cctggagaag aagaggcggc tcctggagaa gctgcaggag cagctggcgc agctgagtgt 1620
51      gcaggccacg gacaaggagg agaacaagca ggtggccctg ggcacgtcca agctcaacta 1680
52      cctggacccc aggatcagca ttgcctggtg caagcgggtt aggggtgccag tggagaagat 1740
53      ctacagcaaaa acacagcggg agaggttcgc ctgggctctc gccatggcag gagaagactt 1800
54      tgaattctaa cgacgagccg tggtgaaact tcttttgtat gtgtgtgtgt ttttttcaact 1860
55      attaaagcag tactggggaa ttttgtacaa taaaaaaaaa aaaaaaaaaa aaaaaaa 1917

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57 &lt;210&gt; SEQ ID NO: 2

58 &lt;211&gt; LENGTH: 601

59 &lt;212&gt; TYPE: PRT

60 &lt;213&gt; ORGANISM: Homo sapiens

61 &lt;400&gt; SEQUENCE: 2

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62      Met Arg Val Val Arg Leu Leu Arg Leu Arg Ala Ala Leu Thr Leu Leu
63      1          5          10          15
64      Gly Glu Val Pro Arg Arg Pro Ala Ser Arg Gly Val Pro Gly Ser Arg
65      20          25          30
66      Arg Thr Gln Lys Gly Ser Gly Ala Arg Trp Glu Lys Glu Lys His Glu
67      35          40          45
68      Asp Gly Val Lys Trp Arg Gln Leu Glu His Lys Gly Pro Tyr Phe Ala
69      50          55          60
70      Pro Pro Tyr Glu Pro Leu Pro Asp Gly Val Arg Phe Phe Tyr Glu Gly
71      65          70          75          80
72      Arg Pro Val Arg Leu Ser Val Pro Ala Glu Glu Val Pro Thr Phe Tyr
73      85          90          95
74      Gly Arg Met Leu Asp His Glu Tyr Thr Lys Glu Val Phe Arg Lys
75      100         105         110
76      Asn Phe Phe Asn Asp Trp Arg Lys Glu Met Ala Val Glu Glu Arg Glu
77      115         120         125
78      Val Ile Lys Ser Leu Asp Lys Cys Asp Phe Thr Glu Ile His Arg Tyr
79      130         135         140
80      Phe Val Asp Lys Ala Ala Ala Arg Lys Val Leu Ser Arg Glu Glu Lys
81      145         150         155         160
82      Gln Lys Leu Lys Glu Glu Ala Glu Lys Leu Gln Gln Glu Phe Gly Tyr
83      165         170         175
84      Cys Ile Leu Asp Gly His Gln Glu Lys Ile Gly Asn Phe Lys Ile Glu
85      180         185         190
86      Pro Pro Gly Leu Phe Arg Gly Arg Gly Asp His Pro Lys Met Gly Met
87      195         200         205
88      Leu Lys Arg Arg Ile Thr Pro Glu Asp Val Val Ile Asn Cys Ser Arg
89      210         215         220
90      Asp Ser Lys Ile Pro Glu Pro Pro Ala Gly His Gln Trp Lys Glu Val
91      225         230         235         240
92      Arg Ser Asp Asn Thr Val Thr Trp Leu Ala Ala Trp Thr Glu Ser Val
93      245         250         255
94      Gln Asn Ser Ile Lys Tyr Ile Met Leu Asn Pro Cys Ser Lys Leu Lys

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95          260          265          270
96 Gly Glu Thr Ala Trp Gln Lys Phe Glu Thr Ala Arg Arg Leu Arg Gly
97          275          280          285
98 Phe Val Asp Glu Ile Arg Ser Gln Tyr Arg Ala Asp Trp Lys Ser Arg
99          290          295          300
100 Glu Met Lys Thr Arg Gln Arg Ala Val Ala Leu Tyr Phe Ile Asp Lys
101          305          310          315          320
102 Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu Asp Gly Glu Ala Ala Asp
103          325          330          335
104 Thr Val Gly Cys Cys Ser Leu Arg Val Glu His Val Gln Leu His Pro
105          340          345          350
106 Glu Ala Asp Gly Cys Gln His Val Val Glu Phe Asp Phe Leu Gly Lys
107          355          360          365
108 Asp Cys Ile Arg Tyr Tyr Asn Arg Val Pro Val Glu Lys Pro Val Tyr
109          370          375          380
110 Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Asp Pro Arg Asp Asp Leu
111          385          390          395          400
112 Phe Asp Arg Leu Thr Thr Thr Ser Leu Asn Lys His Leu Gln Glu Leu
113          405          410          415
114 Met Asp Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr Asn Ala Ser Ile
115          420          425          430
116 Thr Leu Gln Glu Gln Leu Arg Ala Leu Thr Arg Ala Glu Asp Ser Ile
117          435          440          445
118 Ala Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg Val Val Ala Ile
119          450          455          460
120 Leu Cys Asn His Gln Arg Ala Thr Pro Ser Thr Phe Glu Lys Ser Met
121          465          470          475          480
122 Gln Asn Leu Gln Thr Lys Ile Gln Ala Lys Lys Glu Gln Val Ala Glu
123          485          490          495
124 Ala Arg Ala Glu Leu Arg Arg Ala Arg Ala Glu His Lys Ala Gln Gly
125          500          505          510
126 Asp Gly Lys Ser Arg Ser Val Leu Glu Lys Lys Arg Arg Leu Leu Glu
127          515          520          525
128 Lys Leu Gln Glu Gln Leu Ala Gln Leu Ser Val Gln Ala Thr Asp Lys
129          530          535          540
130 Glu Glu Asn Lys Gln Val Ala Leu Gly Thr Ser Lys Leu Asn Tyr Leu
131          545          550          555          560
132 Asp Pro Arg Ile Ser Ile Ala Trp Cys Lys Arg Phe Arg Val Pro Val
133          565          570          575
134 Glu Lys Ile Tyr Ser Lys Thr Gln Arg Glu Arg Phe Ala Trp Ala Leu
135          580          585          590
136 Ala Met Ala Gly Glu Asp Phe Glu Phe
137          595          600
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 23
141 <212> TYPE: DNA
142 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 3
144 cgggatccat gcgcgtgggtg cgg

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Input Set : N:\Crif3\RULE60\10602043.RAW.txt

Output Set: N:\CRF4\07052006\J602043.raw

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146 <210> SEQ ID NO: 4
147 <211> LENGTH: 57
148 <212> TYPE: DNA
149 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 4
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152 <210> SEQ ID NO: 5
153 <211> LENGTH: 633
154 <212> TYPE: PRT
155 <213> ORGANISM: Homo sapiens
156 <400> SEQUENCE: 5
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158      1          5          10          15
159      Pro Lys Lys Ile Lys Thr Glu Asp Thr Lys Lys Glu Lys Lys Arg Lys
160      20          25          30
161      Leu Glu Glu Glu Glu Asp Gly Lys Leu Lys Lys Pro Lys Asn Lys Asp
162      35          40          45
163      Lys Asp Lys Lys Val Pro Glu Pro Asp Asn Lys Lys Lys Lys Pro Lys
164      50          55          60
165      Lys Glu Glu Glu Gln Lys Trp Lys Trp Trp Glu Glu Glu Arg Tyr Pro
166      65          70          75          80
167      Glu Gly Ile Lys Trp Lys Phe Leu Glu His Lys Gly Pro Val Phe Ala
168      85          90          95
169      Pro Pro Tyr Glu Pro Leu Pro Glu Asn Val Lys Phe Tyr Tyr Asp Gly
170      100         105         110
171      Lys Val Met Lys Leu Ser Pro Lys Ala Glu Glu Val Ala Thr Phe Phe
172      115         120         125
173      Ala Lys Met Leu Asp His Glu Tyr Thr Thr Lys Glu Ile Phe Arg Lys
174      130         135         140
175      Asn Phe Phe Lys Asp Trp Arg Lys Glu Met Thr Asn Glu Glu Lys Asn
176      145         150         155         160
177      Ile Ile Thr Asn Leu Ser Lys Cys Asp Phe Thr Gln Met Ser Gln Tyr
178      165         170         175
179      Phe Lys Ala Gln Thr Glu Ala Arg Lys Gln Met Ser Lys Glu Glu Lys
180      180         185         190
181      Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu Leu Lys Glu Tyr Gly Phe
182      195         200         205
183      Cys Ile Met Asp Asn His Lys Glu Arg Ile Ala Asn Phe Lys Ile Glu
184      210         215         220
185      Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn His Pro Lys Met Gly Met
186      225         230         235         240
187      Leu Lys Arg Arg Ile Met Pro Glu Asp Ile Ile Ile Asn Cys Ser Lys
188      245         250         255
189      Asp Ala Lys Val Pro Ser Pro Pro Gly His Lys Trp Lys Glu Val
190      260         265         270
191      Arg His Asp Asn Lys Val Thr Trp Leu Val Ser Trp Thr Glu Asn Ile
192      275         280         285
193      Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn Pro Ser Ser Arg Ile Lys
194      290         295         300

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196 Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr Ala Arg Arg Leu Lys Lys
197 305 310 315 320
198 Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg Glu Asp Trp Lys Ser Lys
199 325 330 335
200 Glu Met Lys Val Arg Gln Arg Ala Val Ala Leu Tyr Phe Ile Asp Lys
201 340 345 350
202 Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu Glu Gly Glu Thr Ala Asp
203 355 360 365
204 Thr Val Gly Cys Cys Ser Leu Arg Val Glu His Ile Asn Leu His Pro
205 370 375 380
206 Glu Leu Asp Gly Gln Glu Tyr Val Val Glu Phe Asp Phe Leu Gly Lys
207 385 390 395 400
208 Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro Val Glu Lys Arg Val Phe
209 405 410 415
210 Lys Asn Leu Gln Leu Phe Met Glu Asn Lys Gln Pro Glu Asp Asp Leu
211 420 425 430
212 Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn Lys His Leu Gln Asp Leu
213 435 440 445
214 Met Glu Gly Leu Thr Ala Lys Val Phe Arg Thr Tyr Asn Ala Ser Ile
215 450 455 460
216 Thr Leu Gln Gln Gln Leu Lys Glu Leu Thr Ala Pro Asp Glu Asn Ile
217 465 470 475 480
218 Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala Asn Arg Ala Val Ala Ile
219 485 490 495
220 Leu Cys Asn His Gln Arg Ala Pro Pro Lys Thr Phe Glu Lys Ser Met
221 500 505 510
222 Met Asn Leu Gln Thr Lys Ile Asp Ala Lys Lys Glu Gln Leu Ala Asp
223 515 520 525
224 Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala Asp Ala Lys Val Met Lys
225 530 535 540
226 Asp Ala Lys Thr Lys Lys Val Val Glu Ser Lys Lys Lys Ala Val Gln
227 545 550 555 560
228 Arg Leu Glu Glu Gln Leu Met Lys Leu Glu Val Gln Ala Thr Asp Arg
229 565 570 575
230 Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr Ser Lys Leu Asn Tyr Leu
231 580 585 590
232 Asp Pro Arg Ile Thr Val Ala Trp Cys Lys Lys Trp Gly Val Pro Ile
233 595 600 605
234 Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu Lys Phe Ala Trp Ala Ile
235 610 615 620
236 Asp Met Ala Asp Glu Asp Tyr Glu Phe
237 625 630

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**VERIFICATION SUMMARY**

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